

when said second binding site is specifically bound by a protein, said first binding site cannot be bound by a protein that otherwise specifically recognizes and binds said first binding site; and

a nucleic acid binding protein that specifically binds said first protein binding site or said second protein binding site.

2. (amended) The system of claim 1, wherein said nucleic acid is a double-stranded nucleic acid.

3. (amended) The system of claim 1, wherein said nucleic acid is a deoxyribonucleic acid (DNA).

4. (amended) The system of claim 1, wherein said first binding site and said second binding site have the same nucleotide sequence.

5. (amended) The system of claim 1, wherein said first binding site and said second binding site have the nucleotide sequence of SEQ ID NO: 1.

6. (amended) The system of claim 1, wherein said first binding site or said second binding site is specifically recognized and bound by a protein selected from the group consisting of Fis, and Tus.

7. (amended) The system of claim 1, wherein said first binding site or said second binding site is bound by EF-tu.

B2 8. (amended) The system of claim 1, wherein said first binding site is within 20 nucleotides of said second binding site.

9. (amended) The system of claim 1, wherein said first binding site is within 11 nucleotides of said second binding site.

10. (amended) The system of claim 8, wherein said first binding site has a strength of at least 2.4 bits as determined by individual information theory.

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11. (amended) The system of claim 1, wherein there is a difference in strength between said first protein binding site and said second protein binding site of more than 0 bits as determined by individual information theory.

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13. (amended) The system of claim 1, wherein:
said first protein binding site is a Fis binding site;
said second protein binding site is a Fis binding site; and
said binding sites are separated from each other by less than 12 nucleotide base pairs.

14. (amended) The system of claim 13, wherein said nucleic acid is a deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.

15. (amended) A composition comprising, an isolated nucleic acid having a length of at least 5 base pairs and having a nucleotide sequence that comprises a first protein binding site, a second protein binding site, and a third protein binding site where said protein binding sites are spaced in proximity to each other such that:

when either said first protein binding site or said third protein binding site is specifically bound by a nucleic acid binding protein, said second binding site cannot be bound by a nucleic acid binding protein that otherwise specifically recognizes and binds said second binding site; and

where said first protein binding site and said third protein binding site can simultaneously be specifically bound by a nucleic acid binding protein.

34. (amended) A composition for the storage of binary information, said composition comprising an isolated nucleic acid having a length of at least 3 base pairs and having a nucleotide sequence that comprises a first protein binding site and a second protein binding site where said first and second protein binding sites are spaced in proximity to each other such that:

when said first protein binding site is specifically bound by a protein, said second binding site cannot be bound by a protein that otherwise specifically recognizes and binds said second binding site; and

when said second binding site is specifically bound by a protein, said first binding site cannot be bound by a protein that otherwise specifically recognizes and binds said first binding site; and

further comprising a nucleic acid binding protein bound to said. first protein binding site or said second protein binding site; wherein binding to the first or the second site is stored binary information.

42. (amended) The composition of claim 34, wherein there is a difference in strength between said first protein binding site and said second protein binding site of more than 0 bits as determined by individual information theory.

51. (amended) A method of storing information, said method comprising the step of:

binding a nucleic acid binding protein to a first protein binding site on a nucleic acid, wherein said nucleic acid has a length of at least 3 base pairs and said nucleic acid comprises said first protein binding site and a second protein binding site where said first and second protein binding sites are spaced in proximity to each other such that:

when said first protein binding site is specifically bound by a protein, said second binding site cannot be bound by a protein that otherwise specifically recognizes and binds said second binding site; and

B6
when said second binding site is specifically bound by a protein,
said first binding site cannot be bound by a protein that otherwise specifically recognizes
and binds said first binding site.

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61. (amended) The method of claim 51, wherein there is a difference
in strength between said first protein binding site and said second protein binding site of
more than 0 bits as determined by individual information theory.

B8
63. (amended) The system of claim 13, wherein said nucleic acid is a
deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.

IN THE ABSTRACT:

Please amend the application to include the abstract on a separate sheet,
which is attached hereto.

REMARKS

Claims 1-65 are pending in the application. Claims 12, 15-33, 43, 64, and
65 are currently withdrawn from consideration by the Examiner as drawn to a non-
elected species. Claims 1-11, 13, 14, 34-42, and 44-63 are currently under examination.
A copy of the pending claims is attached in Appendix B.

Claims 1, 15, 34, and 51 have been amended to recite "comprises" This
amendment adds no new matter and is supported throughout the application. Applicants
note that claim 15 has been amended, even though it is allegedly drawn to a non-elected
species, because it was referred to in the rejection on page 4 regarding the term
"encodes".

Claims 2-11, 13, 14, and 61 have been amended to recite a system. This
amendment adds no new matter and is supported throughout the application.

Claims 11, 42, and 61, have been amended to recite a system, wherein
there is a difference in strength between said first protein binding site and said second
protein binding site of more than at least 0 bits as determined by individual information